

said oligonucleotide does not comprise the iron response element, wherein said molecular interaction site is identified by a method comprising:

comparing the nucleotide sequence of said RNA of a selected organism with the nucleotide sequences of a plurality of nucleic acids from different taxonomic species;

identifying at least one sequence region which is conserved among said plurality of nucleic acids and said RNA of a selected organism;

determining whether said conserved region has secondary structure; and

for said conserved region having secondary structure, identifying said secondary structure.

43. (Amended) The oligonucleotide of claim 35 further comprising comparing said RNA of a selected organism to paralogous nucleic acids.

51. (Amended) An oligonucleotide comprising a molecular interaction site that is present in the RNA of a selected organism and in the RNA of at least one additional organism, wherein said molecular interaction site serves as a binding site for at least one molecule that when bound to said molecular interaction site modulates the expression of said RNA in said selected organism, wherein said oligonucleotide does not comprise the iron response element, wherein said molecular interaction site is identified by a method comprising:

comparing the nucleotide sequence of said RNA of a selected organism with the nucleotide sequences of a plurality of nucleic acids from different taxonomic species, wherein said nucleotide sequence of said RNA of a selected organism is determined by assembling a plurality of expressed sequence tags;

identifying at least one sequence region which is conserved among said plurality of nucleic acids and said RNA of a selected organism;

determining whether said conserved region has secondary structure; and

for said conserved region having secondary structure, identifying said secondary structure.

24 52. (New claim) An oligonucleotide comprising a molecular interaction site that is present in the RNA of a selected organism and in the RNA of at least one additional organism, wherein said molecular interaction site serves as a binding site for at least one molecule that when bound to said molecular interaction site modulates the expression of said RNA in said selected organism, wherein said oligonucleotide does not comprise the iron response element or the 3' untranslated region of the histone mRNA, wherein said molecular interaction site is identified by a method comprising:

comparing the nucleotide sequence of said RNA of a selected organism with the nucleotide sequences of a plurality of nucleic acids from different taxonomic species;

identifying at least one sequence region which is conserved among said plurality of nucleic acids and said RNA of a selected organism;

determining whether said conserved region has secondary structure; and

for said conserved region having secondary structure, identifying said secondary structure.

53. (New claim) The oligonucleotide of claim 52 wherein said method further comprises identifying at least one structural motif for said conserved region having secondary structure.

54. (New claim) The oligonucleotide of claim 53 wherein said method further comprises constructing a set of descriptor elements for said structural motif.

55. (New claim) The oligonucleotide of claim 54 wherein said method further comprises identifying further nucleic acids having secondary structures corresponding to said descriptor elements.

56. (New claim) The oligonucleotide of claim 52 wherein said RNA of a selected organism is present in a eukaryotic cell.

57. (New claim) The oligonucleotide of claim 56 wherein said RNA of a selected organism is selected from the group consisting of mRNA, pre-mRNA, tRNA, rRNA, and snRNA.

58. (New claim) The oligonucleotide of claim 52 wherein said RNA of a selected organism is present in a prokaryotic cell.
59. (New claim) The oligonucleotide of claim 52 further comprising comparing said RNA of a selected organism to paralogous nucleic acids.
60. (New claim) The oligonucleotide of claim 52 wherein said plurality of nucleic acids from different taxonomic species is obtained by performing a sequence similarity search, an ortholog search, or a combination thereof.
61. (New claim) The oligonucleotide of claim 52 wherein said plurality of nucleic acids from different taxonomic species is obtained by performing a sequence similarity search and constructing virtual transcripts.
62. (New claim) The oligonucleotide of claim 52 wherein determining whether said conserved region has secondary structure is performed by self complementarity comparison, alignment and covariance analysis, secondary structure prediction, or a combination thereof.
63. (New claim) The oligonucleotide of claim 62, wherein said secondary structure comprises at least one bulge, loop, stem, hairpin, knot, triple interact, cloverleaf, or helix.
64. (New claim) The oligonucleotide of claim 53 wherein said structural motif is identified by performing self complementarity comparison, alignment and covariance analysis, secondary structure prediction, or a combination thereof.
65. (New claim) The oligonucleotide of claim 54 wherein said set of descriptor elements is constructed using a descriptor database.

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66. (New claim) The oligonucleotide of claim 55 wherein said other nucleic acids having secondary structures corresponding to said descriptor elements are identified by searching at least one database, performing clustering and analysis, searching for orthologs, or a combination thereof.

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67. (New claim) An oligonucleotide comprising a molecular interaction site that is present in the RNA of a selected organism and in the RNA of at least one additional organism, wherein said molecular interaction site serves as a binding site for at least one molecule that when bound to said molecular interaction site modulates the expression of said RNA in said selected organism, wherein said oligonucleotide does not comprise the iron response element or the 3' untranslated region of the histone mRNA, wherein said molecular interaction site is identified by a method comprising:

comparing the nucleotide sequence of said RNA of a selected organism with the nucleotide sequences of a plurality of nucleic acids from different taxonomic species, wherein said nucleotide sequence of said RNA of a selected organism is determined by assembling a plurality of expressed sequence tags;

identifying at least one sequence region which is conserved among said plurality of nucleic acids and said RNA of a selected organism;

determining whether said conserved region has secondary structure; and

for said conserved region having secondary structure, identifying said secondary structure.

REMARKS

Claims 27-29, 35-41 and 43-51 are pending in the present application. Claims 35, 43, and 51 have been amended and claims 52-67 have been added. No new matter has been added. Upon entry of the present amendment, claims 27-29, 35-41 and 43-67 will remain pending.

As a preliminary matter, Applicants acknowledge receipt of the "Attachment for PTO-948" outlining changes for prosecution of applications containing drawings. Formal drawings have been filed on December 13, 2001. Original Figures 6-8, 11, 12, 16, 17, 19, 21-24, 26, 27, 29-65 and 67-97, which are not essential subject matter nor are required to comply with any portion of 35 U.S.C. § 112, have been deleted from the present application. The specification has been amended throughout